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PCT

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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : A01H 1/00, 5/00, C12N 15/00 C12N 9/02, C12P 7/64, 1/02 C12P 1/04, 21/06, C07H 15/12 C07H 17/00	A1	(11) International Publication Number: WO 93/06712 (43) International Publication Date: 15 April 1993 (15.04.93)
(21) International Application Number: PCT/US92/08746 (22) International Filing Date: 13 October 1992 (13.10.92) (30) Priority data: 774,475 10 October 1991 (10.10.91) US 817,919 8 January 1992 (08.01.92) US (60) Parent Application or Grant (63) Related by Continuation US 817,919 (CIP) Filed on 8 January 1992 (08.01.92) (71) Applicant (for all designated States except US): RHONE-POULENC AGROCHIMIE [FR/FR]; 14-20, rue Pierre-Baizet, B.P. 9163, F-69263 Lyon Cédex 09 (FR).		(72) Inventors; and (75) Inventors/Applicants (for US only) : THOMAS, Terry [US/US]; 3004 Normand, College Station, TX 77845 (US). REDDY, Avutu, S. [IN/US]; 3902 E. 29th Street, #G11, Bryan, TX 77802 (US). NUCCIO, Michael [US/US]; P.O. Box 553, College Station, TX 77841 (US). FREYSINET, Georges [FR/FR]; 21, rue de Nervieux, F-Saint-Cyr-au-Mont-d'Or (FR). (74) Agents: SCOTT, Anthony, C. et al.; Scully, Scott, Murphy & Presser, 400 Garden City Plaza, Garden City, NY 11530 (US). (81) Designated States: AU, BG, BR, CA, CS, HU, JP, KR, PL, RO, RU, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE). Published <i>With international search report.</i>
(54) Title: PRODUCTION OF GAMMA LINOLENIC ACID BY A $\Delta 6$ -DESATURASE (57) Abstract Linoleic acid is converted into γ -linolenic acid by the enzyme $\Delta 6$ -desaturase. The present invention is directed to an isolated nucleic acid comprising the $\Delta 6$ -desaturase gene. More particularly, the isolated nucleic acid comprises the promoter, coding region and termination regions of the $\Delta 6$ -desaturase gene. The present invention provides recombinant constructions comprising the $\Delta 6$ -desaturase coding region in functional combination with heterologous regulatory sequences. The nucleic acids and recombinant constructions of the instant invention are useful in the production of GLA in transgenic organisms.		

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PRODUCTION OF GAMMA LINOLENIC ACID
BY A Δ^6 -DESATURASE

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Linoleic acid (18:2) (LA) is transformed into gamma linolenic acid (18:3) (GLA) by the enzyme Δ^6 -desaturase. When this enzyme, or the nucleic acid encoding it, is transferred into LA-producing cells, GLA is produced. The present invention provides a nucleic acid comprising the Δ^6 -desaturase gene. More specifically, the nucleic acid comprises the promoter, coding region and termination regions of the Δ^6 -desaturase gene. The present invention is further directed to recombinant constructions comprising a Δ^6 -desaturase coding region in functional combination with heterologous regulatory sequences. The nucleic acids and recombinant constructions of the instant invention are useful in the production of GLA in transgenic organisms.

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Unsaturated fatty acids such as linoleic ($C_{18}\Delta^{9,12}$) and α -linolenic ($C_{18}\Delta^{9,12,15}$) acids are essential dietary constituents that cannot be synthesized by vertebrates since vertebrate cells can introduce double bonds at the Δ^9 position of fatty acids but cannot introduce additional double bonds between the Δ^9 double bond and the methyl-terminus of the fatty acid chain. Because they are precursors of other products, linoleic and α -linolenic acids are essential fatty acids, and are usually obtained from plant sources. Linoleic acid can be converted by mammals into γ -linolenic acid (GLA, $C_{18}\Delta^{6,9,12}$) which can in turn be converted to arachidonic acid (20:4), a critically important fatty acid since it is an essential precursor of most prostaglandins.

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1 The dietary provision of linoleic acid, by virtue
of its resulting conversion to GLA and arachidonic acid,
satisfies the dietary need for GLA and arachidonic acid.
However, a relationship has been demonstrated between
5 consumption of saturated fats and health risks such as
hypercholesterolemia, atherosclerosis and other chemical
disorders which correlate with susceptibility to
coronary disease, while the consumption of unsaturated
fats has been associated with decreased blood
10 cholesterol concentration and reduced risk of
atherosclerosis. The therapeutic benefits of dietary
GLA may result from GLA being a precursor to arachidonic
acid and thus subsequently contributing to prostaglandin
synthesis. Accordingly, consumption of the more
15 unsaturated GLA, rather than linoleic acid, has
potential health benefits. However, GLA is not present
in virtually any commercially grown crop plant.

Linoleic acid is converted into GLA by the enzyme
 $\Delta 6$ -desaturase. $\Delta 6$ -desaturase, an enzyme of about 359
20 amino acids, has a membrane-bound domain and an active
site for desaturation of fatty acids. When this enzyme
is transferred into cells which endogenously produce
linoleic acid but not GLA, GLA is produced. The present
invention, by providing the gene encoding $\Delta 6$ -desaturase,
25 allows the production of transgenic organisms which
contain functional $\Delta 6$ -desaturase and which produce GLA.
In addition to allowing production of large amounts of
GLA, the present invention provides new dietary sources
of GLA.

30 The present invention is directed to an isolated
 $\Delta 6$ -desaturase gene. Specifically, the isolated gene

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1 comprises the $\Delta 6$ -desaturase promoter, coding region, and termination region.

The present invention is further directed to expression vectors comprising the $\Delta 6$ -desaturase
5 promoter, coding region and termination region.

The present invention is also directed to expression vectors comprising a $\Delta 6$ -desaturase coding region in functional combination with heterologous regulatory regions, i.e. elements not derived from the
10 $\Delta 6$ -desaturase gene.

Cells and organisms comprising the vectors of the present invention, and progeny of such organisms, are also provided by the present invention.

The present invention further provides isolated
15 bacterial $\Delta 6$ -desaturase and is still further directed to an isolated nucleic acid encoding bacterial $\Delta 6$ -desaturase.

The present invention further provides a method for producing plants with increased gamma linolenic acid
20 (GLA) content which comprises transforming a plant cell with an isolated nucleic acid of the present invention and regenerating a plant with increased GLA content from said plant cell.

A method for producing chilling tolerant plants
25 is also provided by the present invention.

Fig. 1 depicts the hydropathy profiles of the deduced amino acid sequences of Synechocystis $\Delta 6$ -desaturase (Panel A) and $\Delta 12$ -desaturase (Panel B). Putative membrane spanning regions are indicated by
30 solid bars. Hydrophobic index was calculated for a window size of 19 amino acid residues [Kyte, et al. (1982) J. Molec. Biol. 157].

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1 Fig. 2 provides gas liquid chromatography
profiles of wild type (Panel A) and transgenic (Panel B)
Anabaena.

5 Fig. 3 is a diagram of maps of cosmid cSy75,
cSy13 and cSy7 with overlapping regions and subclones.
The origins of subclones of cSy75, cSy75-3.5 and cSy7
are indicated by the dashed diagonal lines. Restriction
sites that have been inactivated are in parentheses.

10 Fig. 4 provides gas liquid chromatography
profiles of wild type (Panel A) and transgenic (Panel B)
tobacco.

The present invention provides an isolated
nucleic acid encoding $\Delta 6$ -desaturase. To identify a
nucleic acid encoding $\Delta 6$ -desaturase, DNA is isolated
15 from an organism which produces GLA. Said organism can
be, for example, an animal cell, certain fungi (e.g.
Mortierella), certain bacteria (e.g. Synechocystis) or
certain plants (borage, Oenothera, currants). The
isolation of genomic DNA can be accomplished by a
20 variety of methods well-known to one of ordinary skill
in the art, as exemplified by Sambrook et al. (1989) in
Molecular Cloning: A Laboratory Manual, Cold Spring
Harbor, NY. The isolated DNA is fragmented by physical
methods or enzymatic digestion and cloned into an
25 appropriate vector, e.g. a bacteriophage or cosmid
vector, by any of a variety of well-known methods which
can be found in references such as Sambrook et al.
(1989). Expression vectors containing the DNA of the
present invention are specifically contemplated herein.
30 DNA encoding $\Delta 6$ -desaturase can be identified by gain of
function analysis. The vector containing fragmented DNA
is transferred, for example by infection,

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1 transconjugation, transfection, into a host organism
that produces linoleic acid but not GLA. As used
herein, "transformation" refers generally to the
incorporation of foreign DNA into a host cell. Methods
5 for introducing recombinant DNA into a host organism are
known to one of ordinary skill in the art and can be
found, for example, in Sambrook et al. (1989).
Production of GLA by these organisms (i.e., gain of
function) is assayed, for example by gas chromatography
10 or other methods known to the ordinarily skilled
artisan. Organisms which are induced to produce GLA,
i.e. have gained function by the introduction of the
vector, are identified as expressing DNA encoding $\Delta 6$ -
desaturase, and said DNA is recovered from the
15 organisms. The recovered DNA can again be fragmented,
cloned with expression vectors, and functionally
assessed by the above procedures to define with more
particularity the DNA encoding $\Delta 6$ -desaturase.

As an example of the present invention, random
20 DNA is isolated from the cyanobacteria Synechocystis
Pasteur Culture Collection (PCC) 6803, American Type
Culture Collection (ATCC) 27184, cloned into a cosmid
vector, and introduced by transconjugation into the GLA-
deficient cyanobacterium Anabaena strain PCC 7120, ATCC
25 27893. Production of GLA from Anabaena linoleic acid is
monitored by gas chromatography and the corresponding
DNA fragment is isolated.

The isolated DNA is sequenced by methods well-
known to one of ordinary skill in the art as found, for
30 example, in Sambrook et al. (1989).

In accordance with the present invention, a DNA
comprising a $\Delta 6$ -desaturase gene has been isolated. More

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1 particularly, a 3.588 kilobase (kb) DNA comprising a $\Delta 6$ -
desaturase gene has been isolated from the cyanobacteria
5 Synechocystis. The nucleotide sequence of the 3.588 kb
DNA was determined and is shown in SEQ ID NO:1. Open
reading frames defining potential coding regions are
present from nucleotide 317 to 1507 and from nucleotide
2002 to 3081. To define the nucleotides responsible for
encoding $\Delta 6$ -desaturase, the 3.588 kb fragment that
confers $\Delta 6$ -desaturase activity is cleaved into two
10 subfragments, each of which contains only one open
reading frame. Fragment ORF1 contains nucleotides 1
through 1704, while fragment ORF2 contains nucleotides
1705 through 3588. Each fragment is subcloned in both
forward and reverse orientations into a conjugal
15 expression vector (AM542, Wolk et al. [1984] Proc. Natl.
Acad. Sci. USA 81, 1561) that contains a cyanobacterial
carboxylase promoter. The resulting constructs (i.e.
ORF1(F), ORF1(R), ORF2(F) and ORF2(R)) are conjugated to
wild-type Anabaena PCC 7120 by standard methods (see,
20 for example, Wolk et al. (1984) Proc. Natl. Acad. Sci.
USA 81, 1561). Conjugated cells of Anabaena are
identified as Neo^R green colonies on a brown background
of dying non-conjugated cells after two weeks of growth
on selective media (standard mineral media BG11N +
25 containing 30 μ g/ml of neomycin according to Rippka et
al., (1979) J. Gen Microbiol. 111, 1). The green
colonies are selected and grown in selective liquid
media (BG11N + with 15 μ g/ml neomycin). Lipids are
extracted by standard methods (e.g. Dahmer et al.,
30 (1989) Journal of American Oil Chemical Society 66, 543)
from the resulting transconjugants containing the
forward and reverse oriented ORF1 and ORF2 constructs.

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- 1 For comparison, lipids are also extracted from wild-type cultures of Anabaena and Synechocystis. The fatty acid methyl esters are analyzed by gas liquid chromatography (GLC), for example with a Tracor-560 gas liquid chromatograph equipped with a hydrogen flame ionization detector and a capillary column. The results of GLC analysis are shown in Table 1.

Table 1: Occurrence of C18 fatty acids in wild-type and transgenic cyanobacteria

SOURCE	18:0	18:1	18:2	γ 18:3	α 18:3	18:4
Anabaena (wild type)	+	+	+	-	+	-
Anabaena + ORF1(F)	+	+	+	-	+	-
Anabaena + ORF1(R)	+	+	+	-	+	-
Anabaena + ORF2(F)	+	+	+	+	+	+
Anabaena + ORF2(R)	+	+	+	-	+	-
Synechocystis (wild type)	+	+	+	+	-	-

- As assessed by GLC analysis, GLA deficient Anabaena gain the function of GLA production when the construct containing ORF2 in forward orientation is introduced by transconjugation. Transconjugants containing constructs with ORF2 in reverse orientation to the carboxylase promoter, or ORF1 in either orientation, show no GLA production. This analysis demonstrates that the single open reading frame (ORF2) within the 1884 bp fragment encodes Δ 6-desaturase. The 1884 bp fragment is shown as SEQ ID NO:3. This is substantiated by the overall similarity of the hydropathy profiles between Δ 6-desaturase and Δ 12-

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1 desaturase [Wada et al. (1990) Nature 347] as shown in
Fig. 1 as (A) and (B), respectively.

Isolated nucleic acids encoding $\Delta 6$ -desaturase can
be identified from other GLA-producing organisms by the
5 gain of function analysis described above, or by nucleic
acid hybridization techniques using the isolated nucleic
acid which encodes Anabaena $\Delta 6$ -desaturase as a
hybridization probe. Both genomic and cDNA cloning
methods are known to the skilled artisan and are
10 contemplated by the present invention. The
hybridization probe can comprise the entire DNA sequence
disclosed as SEQ. ID NO:1, or a restriction fragment or
other DNA fragment thereof, including an oligonucleotide
probe. Methods for cloning homologous genes by cross-
15 hybridization are known to the ordinarily skilled
artisan and can be found, for example, in Sambrook
(1989) and Beltz et al. (1983) Methods in Enzymology
100, 266.

Transgenic organisms which gain the function of
20 GLA production by introduction of DNA encoding Δ -
desaturase also gain the function of octadecatetraenoic
acid ($18:4\Delta^{6,9,12,15}$) production. Octadecatetraenoic
acid is present normally in fish oils and in some plant
species of the Boraginaceae family (Craig et al. [1964]
25 J. Amer. Oil Chem. Soc. 41, 209-211; Gross et al. [1976]
Can. J. Plant Sci. 56, 659-664). In the transgenic
organisms of the present invention, octadecatetraenoic
acid results from further desaturation of α -linolenic
acid by $\Delta 6$ -desaturase or desaturation of GLA by $\Delta 15$ -
30 desaturase.

The 359 amino acids encoded by ORF2, i.e. the
open reading frame encoding $\Delta 6$ -desaturase, are shown as

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1 SEQ. ID NO:2. The present invention further
contemplates other nucleotide sequences which encode the
amino acids of SEQ ID NO:2. It is within the ken of the
ordinarily skilled artisan to identify such sequences
5 which result, for example, from the degeneracy of the
genetic code. Furthermore, one of ordinary skill in the
art can determine, by the gain of function analysis
described hereinabove, smaller subfragments of the 1884
bp fragment containing ORF2 which encode $\Delta 6$ -desaturase.

10 The present invention contemplates any such
polypeptide fragment of $\Delta 6$ -desaturase and the nucleic
acids therefor which retain activity for converting LA
to GLA.

In another aspect of the present invention, a
15 vector containing the 1884 bp fragment or a smaller
fragment containing the promoter, coding sequence and
termination region of the $\Delta 6$ -desaturase gene is
transferred into an organism, for example,
cyanobacteria, in which the $\Delta 6$ -desaturase promoter and
20 termination regions are functional. Accordingly,
organisms producing recombinant $\Delta 6$ -desaturase are
provided by this invention. Yet another aspect of this
invention provides isolated $\Delta 6$ -desaturase, which can be
purified from the recombinant organisms by standard
25 methods of protein purification. (For example, see
Ausubel et al. [1987] Current Protocols in Molecular
Biology, Green Publishing Associates, New York).

Vectors containing DNA encoding $\Delta 6$ -desaturase are
also provided by the present invention. It will be
30 apparent to one of ordinary skill in the art that
appropriate vectors can be constructed to direct the
expression of the $\Delta 6$ -desaturase coding sequence in a

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1 variety of organisms. Replicable expression vectors are
particularly preferred. Replicable expression vectors
as described herein are DNA or RNA molecules engineered
for controlled expression of a desired gene, i.e. the
5 $\Delta 6$ -desaturase gene. Preferably the vectors are
plasmids, bacteriophages, cosmids or viruses. Shuttle
vectors, e.g. as described by Wolk et al. (1984) Proc.
Natl. Acad. Sci. USA, 1561-1565 and Bustos et al. (1991)
J. Bacteriol. 174, 7525-7533, are also contemplated in
10 accordance with the present invention. Sambrook et al.
(1989), Goeddel, ed. (1990) Methods in Enzymology 185
Academic Press, and Perbal (1988) A Practical Guide to
Molecular Cloning, John Wiley and Sons, Inc., provide
detailed reviews of vectors into which a nucleic acid
15 encoding the present $\Delta 6$ -desaturase can be inserted and
expressed. Such vectors also contain nucleic acid
sequences which can effect expression of nucleic acids
encoding $\Delta 6$ -desaturase. Sequence elements capable of
effecting expression of a gene product include
20 promoters, enhancer elements, upstream activating
sequences, transcription termination signals and
polyadenylation sites. Both constitutive and tissue
specific promoters are contemplated. For transformation
of plant cells, the cauliflower mosaic virus (CaMV) 35S
25 promoter and promoters which are regulated during plant
seed maturation are of particular interest. All such
promoter and transcriptional regulatory elements, singly
or in combination, are contemplated for use in the
present replicable expression vectors and are known to
30 one of ordinary skill in the art. The CaMV 35S promoter
is described, for example, by Restrepo et al. (1990)

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1 Plant Cell 2, 987. Genetically engineered and mutated
regulatory sequences are also contemplated.

5 The ordinarily skilled artisan can determine
vectors and regulatory elements suitable for expression
in a particular host cell. For example, a vector
comprising the promoter from the gene encoding the
carboxylase of Anabaena operably linked to the coding
region of $\Delta 6$ -desaturase and further operably linked to a
termination signal from Synechocystis is appropriate for
10 expression of $\Delta 6$ -desaturase in cyanobacteria. "Operably
linked" in this context means that the promoter and
terminator sequences effectively function to regulate
transcription. As a further example, a vector
appropriate for expression of $\Delta 6$ -desaturase in
15 transgenic plants can comprise a seed-specific promoter
sequence derived from helianthinin, napin, or glycin
operably linked to the $\Delta 6$ -desaturase coding region and
further operably linked to a seed termination signal or
the nopaline synthase termination signal.

20 In particular, the helianthinin regulatory
elements disclosed in applicant's copending U.S.
Application Serial No. 682,354, filed April 8, 1991 and
incorporated herein by reference, are contemplated as
promoter elements to direct the expression of the $\Delta 6$ -
25 desaturase of the present invention.

Modifications of the nucleotide sequences or
regulatory elements disclosed herein which maintain the
functions contemplated herein are within the scope of
this invention. Such modifications include insertions,
30 substitutions and deletions, and specifically
substitutions which reflect the degeneracy of the
genetic code.

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1 Standard techniques for the construction of such
hybrid vectors are well-known to those of ordinary skill
in the art and can be found in references such as
Sambrook et al. (1989), or any of the myriad of
5 laboratory manuals on recombinant DNA technology that
are widely available. A variety of strategies are
available for ligating fragments of DNA, the choice of
which depends on the nature of the termini of the DNA
fragments. It is further contemplated in accordance
10 with the present invention to include in the hybrid
vectors other nucleotide sequence elements which
facilitate cloning, expression or processing, for
example sequences encoding signal peptides, a sequence
encoding KDEL, which is required for retention of
15 proteins in the endoplasmic reticulum or sequences
encoding transit peptides which direct $\Delta 6$ -desaturase to
the chloroplast. Such sequences are known to one of
ordinary skill in the art. An optimized transit peptide
is described, for example, by Van den Broeck et al.
20 (1985) Nature 313, 358. Prokaryotic and eukaryotic
signal sequences are disclosed, for example, by
Michaelis et al. (1982) Ann. Rev. Microbiol. 36, 425.

A further aspect of the instant invention
provides organisms other than cyanobacteria which
25 contain the DNA encoding the $\Delta 6$ -desaturase of the
present invention. The transgenic organisms
contemplated in accordance with the present invention
include bacteria, cyanobacteria, fungi, and plants and
animals. The isolated DNA of the present invention can
30 be introduced into the host by methods known in the art,
for example infection, transfection, transformation or
transconjugation. Techniques for transferring the DNA

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1 of the present invention into such organisms are widely
known and provided in references such as Sambrook et al.
(1989).

A variety of plant transformation methods are
5 known. The $\Delta 6$ -desaturase gene can be introduced into
plants by a leaf disk transformation-regeneration
procedure as described by Horsch et al. (1985) Science
227, 1229. Other methods of transformation, such as
protoplast culture (Horsch et al. (1984) Science 223,
10 496; DeBlock et al. (1984) EMBO J. 2, 2143; Barton et
al. (1983) Cell 32, 1033) can also be used and are
within the scope of this invention. In a preferred
embodiment plants are transformed with Agrobacterium-
derived vectors. However, other methods are available
15 to insert the $\Delta 6$ -desaturase gene of the present
invention into plant cells. Such alternative methods
include biolistic approaches (Klein et al. (1987) Nature
327, 70), electroporation, chemically-induced DNA
uptake, and use of viruses or pollen as vectors.

20 When necessary for the transformation method, the
 $\Delta 6$ -desaturase gene of the present invention can be
inserted into a plant transformation vector, e.g. the
binary vector described by Bevan (1984) Nucleic Acids
Res. 12, 8111. Plant transformation vectors can be
25 derived by modifying the natural gene transfer system of
Agrobacterium tumefaciens. The natural system comprises
large Ti (tumor-inducing)-plasmids containing a large
segment, known as T-DNA, which is transferred to
transformed plants. Another segment of the Ti plasmid,
30 the vir region, is responsible for T-DNA transfer. The
T-DNA region is bordered by terminal repeats. In the
modified binary vectors the tumor-inducing genes have

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1 been deleted and the functions of the vir region are
utilized to transfer foreign DNA bordered by the T-DNA
border sequences. The T-region also contains a
selectable marker for antibiotic resistance, and a
5 multiple cloning site for inserting sequences for
transfer. Such engineered strains are known as
"disarmed" A. tumefaciens strains, and allow the
efficient transformation of sequences bordered by the T-
region into the nuclear genomes of plants.

10 Surface-sterilized leaf disks are inoculated with
the "disarmed" foreign DNA-containing A. tumefaciens,
cultured for two days, and then transferred to
antibiotic-containing medium. Transformed shoots are
selected after rooting in medium containing the
15 appropriate antibiotic, transferred to soil and
regenerated.

Another aspect of the present invention provides
transgenic plants or progeny of these plants containing
the isolated DNA of the invention. Both
20 monocotyledenous and dicotyledenous plants are
contemplated. Plant cells are transformed with the
isolated DNA encoding $\Delta 6$ -desaturase by any of the plant
transformation methods described above. The transformed
plant cell, usually in a callus culture or leaf disk, is
25 regenerated into a complete transgenic plant by methods
well-known to one of ordinary skill in the art (e.g.
Horsch et al. (1985) Science 227, 1129). In a preferred
embodiment, the transgenic plant is sunflower, oil seed
rape, maize, tobacco, peanut or soybean. Since progeny
30 of transformed plants inherit the DNA encoding $\Delta 6$ -
desaturase, seeds or cuttings from transformed plants
are used to maintain the transgenic plant line.

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1 The present invention further provides a method
for providing transgenic plants with an increased
content of GLA. This method includes introducing DNA
encoding $\Delta 6$ -desaturase into plant cells which lack or
5 have low levels of GLA but contain LA, and regenerating
plants with increased GLA content from the transgenic
cells. In particular, commercially grown crop plants
are contemplated as the transgenic organism, including,
but not limited to, sunflower, soybean, oil seed rape,
10 maize, peanut and tobacco.

 The present invention further provides a method
for providing transgenic organisms which contain GLA.
This method comprises introducing DNA encoding $\Delta 6$ -
desaturase into an organism which lacks or has low
15 levels of GLA, but contains LA. In another embodiment,
the method comprises introducing one or more expression
vectors which comprise DNA encoding $\Delta 12$ -desaturase and
 $\Delta 6$ -desaturase into organisms which are deficient in both
GLA and LA. Accordingly, organisms deficient in both LA
20 and GLA are induced to produce LA by the expression of
 $\Delta 12$ -desaturase, and GLA is then generated due to the
expression of $\Delta 6$ -desaturase. Expression vectors
comprising DNA encoding $\Delta 12$ -desaturase, or $\Delta 12$ -
desaturase and $\Delta 6$ -desaturase, can be constructed by
25 methods of recombinant technology known to one of
ordinary skill in the art (Sambrook et al., 1989) and
the published sequence of $\Delta 12$ -desaturase (Wada et al
[1990] Nature (London) 347, 200-203. In addition, it
has been discovered in accordance with the present
30 invention that nucleotides 2002-3081 of SEQ. ID NO:1
encode cyanobacterial $\Delta 12$ -desaturase. Accordingly, this
sequence can be used to construct the subject expression

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1 vectors. In particular, commercially grown crop plants
are contemplated as the transgenic organism, including,
but not limited to, sunflower, soybean, oil seed rape,
maize, peanut and tobacco.

5 The present invention is further directed to a
method of inducing chilling tolerance in plants.
Chilling sensitivity may be due to phase transition of
lipids in cell membranes. Phase transition temperature
depends upon the degree of unsaturation of fatty acids
10 in membrane lipids, and thus increasing the degree of
unsaturation, for example by introducing $\Delta 6$ -desaturase
to convert LA to GLA, can induce or improve chilling
resistance. Accordingly, the present method comprises
introducing DNA encoding $\Delta 6$ -desaturase into a plant
15 cell, and regenerating a plant with improved chilling
resistance from said transformed plant cell. In a
preferred embodiment, the plant is a sunflower, soybean,
oil seed rape, maize, peanut or tobacco plant.

20 The following examples further illustrate the
present invention..

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EXAMPLE 1

Strains and Culture Conditions

Synechocystis (PCC 6803, ATCC 27184), Anabaena (PCC 7120, ATCC 27893) and Synechococcus (PCC 7942, ATCC 33912) were grown photoautotrophically at 30°C in BG11N+ medium (Rippka et al. [1979] J. Gen. Microbiol. 111, 1-61) under illumination of incandescent lamps ($60\mu\text{E.m}^{-2}.\text{S}^{-1}$). Cosmids and plasmids were selected and propagated in Escherichia coli strain DH5a on LB medium supplemented with antibiotics at standard concentrations as described by Maniatis et al. (1982) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring, New York.

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EXAMPLE 2

Construction of Synechocystis Cosmid Genomic Library

Total genomic DNA from Synechocystis (PCC 6803) was partially digested with Sau3A and fractionated on a sucrose gradient (Ausubel et al. [1987] Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, New York). Fractions containing 30 to 40 kb DNA fragments were selected and ligated into the dephosphorylated BamHI site of the cosmid vector, pDUCA7 (Buikema et al. [1991] J. Bacteriol. 173, 1879-1885). The ligated DNA was packaged in vitro as described by Ausubel et al. (1987), and packaged phage were propagated in E. coli DH5 α containing the AvaI and Eco4711 methylase helper plasmid, pRL528 as described by Buikema et al. (1991). A total of 1152 colonies were isolated randomly and maintained individually in twelve 96-well microtiter plates.

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EXAMPLE 3

Gain-of-Function Expression of GLA in Anabaena

Anabaena (PCC 7120), a filamentous cyanobacterium, is deficient in GLA but contains significant amounts of linoleic acid, the precursor for GLA (Figure 2; Table 2). The Synechocystis cosmid library described in Example 2 was conjugated into Anabaena (PCC 7120) to identify transconjugants that produce GLA. Anabaena cells were grown to mid-log phase in BG11N+ liquid medium and resuspended in the same medium to a final concentration of approximately 2×10^8 cells per ml. A mid-log phase culture of E. coli RP4 (Burkardt et al. [1979] J. Gen. Microbiol. 114, 341-348) grown in LB containing ampicillin was washed and resuspended in fresh LB medium. Anabaena and RP4 were then mixed and spread evenly on BG11N+ plates containing 5% LB. The cosmid genomic library was replica plated onto LB plates containing 50 μ g/ml kanamycin and 17.5 μ g/ml chloramphenicol and was subsequently patched onto BG11N+ plates containing Anabaena and RP4. After 24 hours of incubation at 30°C, 30 μ g/ml of neomycin was underlaid; and incubation at 30°C was continued until transconjugants appeared.

Individual transconjugants were isolated after conjugation and grown in 2 ml BG11N+ liquid medium with 15 μ g/ml neomycin. Fatty acid methyl esters were prepared from wild type cultures and cultures containing pools of ten transconjugants as follows. Wild type and transgenic cyanobacterial cultures were harvested by centrifugation and washed twice with distilled water. Fatty acid methyl esters were extracted from these cultures as described by Dahmer et al. (1989) J. Amer.

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1 Oil. Chem. Soc. 66, 543-548 and were analyzed by Gas
Liquid Chromatography (GLC) using a Tracor-560 equipped
with a hydrogen flame ionization detector and capillary
5 column (30 m x 0.25 mm bonded FSOT Superox II, Alltech
Associates Inc., IL). Retention times and co-
chromatography of standards (obtained from Sigma
Chemical Co.) were used for identification of fatty
acids. The average fatty acid composition was
determined as the ratio of peak area of each C18 fatty
10 acid normalized to an internal standard.

Representative GLC profiles are shown in Fig. 2.
C18 fatty acid methyl esters are shown. Peaks were
identified by comparing the elution times with known
standards of fatty acid methyl esters and were confirmed
15 by gas chromatography-mass spectrometry. Panel A
depicts GLC analysis of fatty acids of wild type
Anabaena. The arrow indicates the migration time of
GLA. Panel B is a GLC profile of fatty acids of
transconjugants of Anabaena with pAM542+1.8F. Two GLA
20 producing pools (of 25 pools representing 250
transconjugants) were identified that produced GLA.
Individual transconjugants of each GLA positive pool
were analyzed for GLA production; two independent
transconjugants, AS13 and AS75, one from each pool, were
25 identified which expressed significant levels of GLA and
which contained cosmids, cSy13 and cSy75, respectively
(Figure 3). The cosmids overlap in a region
approximately 7.5 kb in length. A 3.5 kb NheI fragment
of cSy75 was recloned in the vector pDUCA7 and
30 transferred to Anabaena resulting in gain-of-function
expression of GLA (Table 2).

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1 Two NheI/Hind III subfragments (1.8 and 1.7 kb)
of the 3.5 kb Nhe I fragment of cSy75-3.5 were subcloned
into "pBLUESCRIPT" (Stratagene) (Figure 3) for
sequencing. Standard molecular biology techniques were
5 performed as described by Maniatis et al. (1982) and
Ausubel et al. (1987). Dideoxy sequencing (Sanger et al.
[1977] Proc. Natl. Acad. Sci. USA 74, 5463-5467) of
pBS1.8 was performed with "SEQUENASE" (United States
Biochemical) on both strands by using specific
10 oligonucleotide primers synthesized by the Advanced DNA
Technologies Laboratory (Biology Department, Texas A & M
University). DNA sequence analysis was done with the
GCG (Madison, WI) software as described by Devereux et
al. (1984) Nucleic Acids Res. 12, 387-395.

15 Both NheI/HindIII subfragments were transferred
into a conjugal expression vector, AM542, in both
forward and reverse orientations with respect to a
cyanobacterial carboxylase promoter and were introduced
into Anabaena by conjugation. Transconjugants
20 containing the 1.8 kb fragment in the forward
orientation (AM542-1.8F) produced significant quantities
of GLA and octadecatetraenoic acid (Figure 2; Table 2).
Transconjugants containing other constructs, either
reverse oriented 1.8 kb fragment or forward and reverse
25 oriented 1.7 kb fragment, did not produce detectable
levels of GLA (Table 2).

Figure 2 compares the C18 fatty acid profile of
an extract from wild type Anabaena (Figure 2A) with that
of transgenic Anabaena containing the 1.8 kb fragment of
30 cSy75-3.5 in the forward orientation (Figure 2B). GLC
analysis of fatty acid methyl esters from AM542-1.8F
revealed a peak with a retention time identical to that

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- 1 of authentic GLA standard. Analysis of this peak by gas chromatography-mass spectrometry (GC-MS) confirmed that it had the same mass fragmentation pattern as a GLA reference sample. Transgenic Anabaena with altered
- 5 levels of polyunsaturated fatty acids were similar to wild type in growth rate and morphology.

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Table 2
Composition of C18 Fatty Acids in
Wild Type and Trasgenic Cyanobacteria

Strain	Fatty acid (%)					
	18:0	18:1	18:2	18:3 (α)	18:3 (γ)	18:4
Wild type						
Synechocystis (sp.PCC6803)	13.6	4.5	54.5	-	27.3	-
Anabaena (sp.PCC7120)	2.9	24.8	37.1	35.2	-	-
Synechococcus (Sp.PCC7942)	20.6	79.4	-	-	-	-
Anabaena Transconjugants						
cSy75	3.8	24.4	22.3	9.1	27.9	12.5
cSy75-3.5	4.3	27.6	18.1	3.2	40.4	6.4
pAM542-1.8F	4.2	13.9	12.1	19.1	25.4	25.4
pAM542-1.8R	7.7	23.1	38.4	30.8	-	-
pAM542-1.7F	2.8	27.8	36.1	33.3	-	-
pAM542-1.7R	2.8	25.4	42.3	29.6	-	-
Synechococcus Transformants						
pAM854	27.8	72.2	-	-	-	-
pAM854- Δ^{12}	4.0	43.2	46.0	-	-	-
pAM854- Δ^6	18.2	81.8	-	-	-	-
pAM854- Δ^6 & Δ^{12}	42.7	25.3	19.5	-	16.5	-

18:0, stearic acid; 18:1, oleic acid; 18:2, linoleic
acid; 18:3(α), α -linolenic acid; 18:3(γ), γ -linolenic
acid; 18:4, octadecatetraenoic acid

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EXAMPLE 4

Transformation of Synechococcus
with $\Delta 6$ and $\Delta 12$ Desaturase Genes

5 A third cosmid, cSy7, which contains a $\Delta 12$ -
desaturase gene, was isolated by screening the
Synechocystis genomic library with a oligonucleotide
synthesized from the published Synechocystis $\Delta 12$ -
desaturase gene sequence (Wada et al. [1990] Nature
10 (London) 347, 200-203). A 1.7 kb AvaI fragment from
this cosmid containing the $\Delta 12$ -desaturase gene was
identified and used as a probe to demonstrate that cSy13
not only contains a $\Delta 6$ -desaturase gene but also a $\Delta 12$ -
desaturase gene (Figure 3). Genomic Southern blot
analysis further showed that both the $\Delta 6$ -and $\Delta 12$ -
15 desaturase genes are unique in the Synechocystis genome
so that both functional genes involved in C18 fatty acid
desaturation are linked closely in the Synechocystis
genome.

The unicellular cyanobacterium Synechococcus (PCC
20 7942) is deficient in both linoleic acid and GLA(3).
The $\Delta 12$ and $\Delta 6$ -desaturase genes were cloned individually
and together into pAM854 (Bustos et al. [1991] J.
Bacteriol. 174, 7525-7533), a shuttle vector that
contains sequences necessary for the integration of
foreign DNA into the genome of Synechococcus (Golden et
25 al. [1987] Methods in Enzymol. 153, 215-231).
Synechococcus was transformed with these gene constructs
and colonies were selected. Fatty acid methyl esters
were extracted from transgenic Synechococcus and
30 analyzed by GLC.

Table 2 shows that the principal fatty acids of
wild type Synechococcus are stearic acid (18:0) and

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1 oleic acid (18:1). Synechococcus transformed with
pAM854- Δ 12 expressed linoleic acid (18:2) in addition to
the principal fatty acids. Transformants with pAM854- Δ 6
and Δ 12 produced both linoleate and GLA (Table 1).
5 These results indicated that Synechococcus containing
both Δ 12- and Δ 6-desaturase genes has gained the
capability of introducing a second double bond at the
 Δ 12 position and a third double bond at the Δ 6 position
of C18 fatty acids. However, no changes in fatty acid
10 composition was observed in the transformant containing
pAM854- Δ 6, indicating that in the absence of substrate
synthesized by the Δ 12 desaturase, the Δ 6-desaturase is
inactive. This experiment further confirms that the 1.8
kb NheI/HindIII fragment (Figure 3) contains both coding
15 and promoter regions of the Synechocystis Δ 6-desaturase
gene. Transgenic Synechococcus with altered levels of
polyunsaturated fatty acids were similar to wild type in
growth rate and morphology.

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EXAMPLE 5

Nucleotide Sequence of $\Delta 6$ -Desaturase

The nucleotide sequence of the 1.8 kb fragment of cSy75-3.5 including the functional $\Delta 6$ -desaturase gene was determined. An open reading frame encoding a polypeptide of 359 amino acids was identified (Figure 4). A Kyte-Doolittle hydrophathy analysis (Kyte et al. [1982] J. Mol. Biol. 157, 105-132) identified two regions of hydrophobic amino acids that could represent transmembrane domains (Figure 1A); furthermore, the hydrophathic profile of the $\Delta 6$ -desaturase is similar to that of the $\Delta 12$ -desaturase gene (Figure 1B; Wada et al.) and $\Delta 9$ -desaturases (Thiede et al. [1986] J. Biol. Chem. 261, 13230-13235). However, the sequence similarity between the Synechocystis $\Delta 6$ - and $\Delta 12$ -desaturases is less than 40% at the nucleotide level and approximately 18% at the amino acid level.

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EXAMPLE 6

Transfer of Cyanobacterial Δ^6 -Desaturase into Tobacco

The cyanobacterial Δ^6 -desaturase gene was mobilized into a plant expression vector and transferred to tobacco using Agrobacterium mediated gene transfer techniques. To ensure that the transferred desaturase is appropriately expressed in leaves and developing seeds and that the desaturase gene product is targeted to the endoplasmic reticulum or the chloroplast, various expression cassettes with Synechocystis Δ -desaturase open reading frame (ORF) were constructed. Components of these cassettes include: (i) a 35S promoter or seed specific promoter derived from the sunflower helianthinin gene to drive Δ^6 -desaturase gene expression in all plant tissues or only in developing seeds respectively, (ii) a putative signal peptide either from carrot extensin gene or sunflower helianthinin gene to target newly synthesized Δ^6 -desaturase into the ER, (iii) an ER lumen retention signal sequence (KDEL) at the COOH-terminal of the Δ^6 -desaturase ORF, and (iv) an optimized transit peptide to target Δ^6 desaturase into the chloroplast. The 35S promoter is a derivative of PRTL2 described by Restrepo et al. (1990). The optimized transit peptide sequence is described by Van de Broeck et al. (1985). The carrot extensin signal peptide is described by Chen et al. (1985) EMBO J. 9, 2145.

Transgenic tobacco plants were produced containing a chimeric cyanobacterial desaturase gene, comprised of the Synechocystis Δ^6 desaturase gene fused to an endoplasmic reticulum retention sequence (KDEL) and extensin signal peptide driven by the CaMV 35S promoter. PCR amplifications of transgenic tobacco genomic DNA indicate that the Δ^6 desaturase gene was incorporated into the tobacco genome. Fatty acid methyl esters of leaves of these transgenic tobacco plants were

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1 extracted and analyzed by Gas Liquid Chromatography
(GLC). These transgenic tobacco accumulated significant
amounts of GLA (Figure 4). Figure 4 shows fatty acid
methyl esters as determined by GLC. Peaks were
5 identified by comparing the elution times with known
standards of fatty acid methyl ester. Accordingly,
cyanobacterial genes involved in fatty acid metabolism
can be used to generate transgenic plants with altered
fatty acid compositions.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Thomas, Terry L.
Reddy, Avutu S.
Nuccio, Michael
Freyssinet, Georges L.

(ii) TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC
ACID BY A DELTA 6-DESATURASE

10

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

15

(A) ADDRESSEE: Scully, Scott, Murphy & Presser
(B) STREET: 400 Garden City Plaza
(C) CITY: Garden City
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 11530

(v) COMPUTER READABLE FORM:

20

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: 08-JAN-1992
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

25

(A) NAME: McNulty, William E.
(B) REGISTRATION NUMBER: 22,606
(C) REFERENCE/DOCKET NUMBER: 83832

(ix) TELECOMMUNICATION INFORMATION:

30

(A) TELEPHONE: (516) 742-4343
(B) TELEFAX: (516) 742-4366
(C) TELEX: 230 901 SANS UR

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-30-

1

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2002..3081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCC GTATTCTGAA	60
	TCCCCGCATT CGCATTGTTA ATCGTTTGTT CAACCATGCC CTGGGTAAAC GTTTAGACAC	120
	CACCTTGCCA GACCACGTTA GTTTGAGTGT TTCCGCCCTG GCGGCCCCGA TTTTTTCCIT	180
	TGCGGCTTTG GGCAATCAGG CGATCGGGCA ATTGCGTTTG TTGACCAGA CTGGGCCCAT	240
	TCAGGAAATT GTCATTCACC AAGACCATCC CTGGCTCAAT TTACCCCTGG CGGATTTATG	300
15	GGATGATCCG AGCCGAATGT TGATCTATTA CCTACCGGCC CACAGTGAAA CGGATTTAGT	360
	AGGCGCAGTG GTGAATAATT TAACGTTGCA ATCTGGGGAC CATTTAATAG TGGGACAAAA	420
	ACCCCAACCC AAGACCAAAC GGCGATCGCC TTGGCGCAAA TTTTCCAAAC TGATTACCAA	480
	CCTGCGGGAG TATCAGCGGT ATGTCCAACA GGTGATATGG GTGGTGTGT TTTTATTGTT	540
	GATGATTTTT CTGGCCACCT TCATCTACGT TTCCATTGAT CAACATATTG CCCCAGTGGA	600
20	CGCGTTGTAT TTTTCCGTGG GCATGATTAC CGGGGCCGGT GGCAAGGAAG AGGTGGCCGA	660
	AAAGTCCCCC GATATCATCA AAGTATTCAC AGTGGTGATG ATGATCGCCG GGGCGGGGGT	720
	GATTGGTATT TGTATGCCC TACTGAATGA TTTTCATCCTT GGCAGTCGCT TTAGTCAGTT	780
	TTTGGATGCG GCCAAGTTAC CCGATCGCCA TCACATCATC ATTTGTGGGC TGGGGGGAGT	840
25	GAGCATGGCC ATTATTGAAG AGTTAATTCA CCAGGGCCAT GAAATTGTGG TAATCGAAAA	900
	GGATACAGAT AATCGTTTCT TGCATACGGC CCGCTCCCTG GGGGTGCCCC TAATTGTGGA	960

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1	GGATGCCCGC	CTAGAAAGAA	CGTTGGCCTG	CGCCAATATC	AACCGAGCCG	AAGCCATTGT	1020										
	GGTGGCCACC	AGCGACGACA	CCGTTAACTT	GGAAATTGGC	CTAACTGCCA	AGGCGATCGC	1080										
	CCCTAGCCTG	CCAGTGGTGT	TGCGTTGCCA	GGATGCCCAG	TTTAGCCTGT	CCCTGCAGGA	1140										
	AGTATTTGAA	TTTGAAACGG	TGCTTTGTCC	GGCGGAATTG	GCCACCTATT	CCTTTGCGGC	1200										
5	GGCGGCCCTG	GGGGGCAAAA	TTTTGGGCAA	CGGCATGACC	GATGATTTCG	TGTGGGTAGC	1260										
	CCTAGCCACC	TTAATCACTC	CTAACCATCC	CTTTGCCGAC	CAATTGGTTA	AAATTGCAGC	1320										
	CCAAAAGTCT	GATTTTCGTC	CCCTCTATCT	AGAACGGGGT	GGCAAAACCA	TCCATAGCTG	1380										
	GGAATTATTG	GGTACCCATC	TCGACTCTGG	AGACGTGTTG	TATTTAACCA	TGCCCGCCAC	1440										
10	TGCCCTAGAG	CAACTTTGGC	GATCGCCCCG	TGCCACTGCT	GATCCTCTGG	ACTCTTTTTT	1500										
	GGTTTAGCAT	GGGGGGATGG	AACTCTTGAC	TCGGCCCAAT	GGTGATCAAG	AAAGAACGCT	1560										
	TTGTCTATGT	TTAGTATTTT	TAAGTTAACC	AACAGCAGAG	GATAACTTCC	AAAAGAAATT	1620										
	AAGCTCAAAA	AGTAGCAAAA	TAAGTTTAAT	TCATAACTGA	GTTTTACTGC	TAAACAGCGG	1680										
	TGCAAAAAAG	TCAGATAAAA	TAAAAGCTTC	ACTTCGGTTT	TATATTGTGA	CCATGGTTCC	1740										
15	CAGGCATCTG	CTCTAGGGAG	TTTTTCCGCT	GCCTTTAGAG	AGTATTTTCT	CCAAGTCGGC	1800										
	TAACTCCCCC	ATTTTtaggc	AAAATCATAT	ACAGACTATC	CCAATATTGC	CAGAGCTTTG	1860										
	ATGACTCACT	GTAGAAGGCA	GACTAAAATT	CTAGCAATGG	ACTCCCAGTT	GGAATAAATT	1920										
	TTTAGTCTCC	CCCGGCGCTG	GAGTTTTTTT	GTAGTTAATG	GCGGTATAAT	GTGAAAGTTT	1980										
20	TTTATCTATT	TAAATTTATA	A	ATG	CTA	ACA	GCG	GAA	AGA	ATT	AAA	TTT	ACC	2031			
			Met	Leu	Thr	Ala	Glu	Arg	Ile	Lys	Phe	Thr					
			1				5					10					
	CAG	AAA	CGG	GGG	TTT	CGT	CGG	GTA	CTA	AAC	CAA	CGG	GTG	GAT	GCC	TAC	2079
	Gln	Lys	Arg	Gly	Phe	Arg	Arg	Val	Leu	Asn	Gln	Arg	Val	Asp	Ala	Tyr	
				15						20					25		
	TTT	GCC	GAG	CAT	GGC	CTG	ACC	CAA	AGG	GAT	AAT	CCC	TCC	ATG	TAT	CTG	2127
	Phe	Ala	Glu	His	Gly	Leu	Thr	Gln	Arg	Asp	Asn	Pro	Ser	Met	Tyr	Leu	
				30					35					40			

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1	AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG GCC TTT GTG Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp Ala Phe Val 45 50 55	2175
	CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC CTA CTG GGT TGT ATG GTT Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Leu Gly Cys Met Val 60 65 70	2223
5	TTG GCG ATC GCC TTG GCG GCC TTT TCC TTC AAT GTC GGC CAC GAT GCC Leu Ala Ile Ala Leu Ala Ala Phe Ser Phe Asn Val Gly His Asp Ala 75 80 85 90	2271
	AAC CAC AAT GCC TAT TCC TCC AAT CCC CAC ATC AAC CGG GTT CTG GGC Asn His Asn Ala Tyr Ser Ser Asn Pro His Ile Asn Arg Val Leu Gly 95 100 105	2319
10	ATG ACC TAC GAT TTT GTC GGG TTA TCT AGT TTT CTT TGG CGC TAT CGC Met Thr Tyr Asp Phe Val Gly Leu Ser Ser Phe Leu Trp Arg Tyr Arg 110 115 120	2367
	CAC AAC TAT TTG CAC CAC ACC TAC ACC AAT ATT CTT GGC CAT GAC GTG His Asn Tyr Leu His His Thr Tyr Thr Asn Ile Leu Gly His Asp Val 125 130 135	2415
	GAA ATC CAT GGA GAT GGC GCA GTA CGT ATG AGT CCT GAA CAA GAA CAT Glu Ile His Gly Asp Gly Ala Val Arg Met Ser Pro Glu Gln Glu His 140 145 150	2463
15	GTT GGT ATT TAT CGT TTC CAG CAA TTT TAT ATT TGG GGT TTA TAT CTT Val Gly Ile Tyr Arg Phe Gln Gln Phe Tyr Ile Trp Gly Leu Tyr Leu 155 160 165	2511
	TTC ATT CCC TTT TAT TGG TTT CTC TAC GAT GTC TAC CTA GTG CTT AAT Phe Ile Pro Phe Tyr Trp Phe Leu Tyr Asp Val Tyr Leu Val Leu Asn 175 180 185	2559
20	AAA GGC AAA TAT CAC GAC CAT AAA ATT CCT CCT TTC CAG CCC CTA GAA Lys Gly Lys Tyr His Asp His Lys Ile Pro Pro Phe Gln Pro Leu Glu 190 195 200	2607
	TTA GCT AGT TTG CTA GGG ATT AAG CTA TTA TGG CTC GGC TAC GTT TTC Leu Ala Ser Leu Leu Gly Ile Lys Leu Leu Trp Leu Gly Tyr Val Phe 205 210 215	2655
25	GGC TTA CCT CTG GCT CTG GGC TTT TCC ATT CCT GAA GTA TTA ATT GGT Gly Leu Pro Leu Ala Leu Gly Phe Ser Ile Pro Glu Val Leu Ile Gly 220 225 230	2703

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1	GCT TCG GTA ACC TAT ATG ACC TAT GGC ATC GTG GTT TGC ACC ATC TTT Ala Ser Val Thr Tyr Met Thr Tyr Gly Ile Val Val Cys Thr Ile Phe 235 240 245 250	2751
	ATG CTG GCC CAT GTG TTG GAA TCA ACT GAA TTT CTC ACC CCC GAT GGT Met Leu Ala His Val Leu Glu Ser Thr Glu Phe Leu Thr Pro Asp Gly 255 260 265	2799
5	GAA TCC GGT GCC ATT GAT GAC GAG TGG GCT ATT TGC CAA ATT CGT ACC Glu Ser Gly Ala Ile Asp Asp Glu Trp Ala Ile Cys Gln Ile Arg Thr 270 275 280	2847
	ACG GCC AAT TTT GCC ACC AAT AAT CCC TTT TGG AAC TGG TTT TGT GGC Thr Ala Asn Phe Ala Thr Asn Asn Pro Phe Trp Asn Trp Phe Cys Gly 285 290 295	2895
10	GGT TTA AAT CAC CAA GTT ACC CAC CAT CTT TTC CCC AAT ATT TGT CAT Gly Leu Asn His Gln Val Thr His His Leu Phe Pro Asn Ile Cys His 300 305 310	2943
	ATT CAC TAT CCC CAA TTG GAA AAT ATT ATT AAG GAT GTT TGC CAA GAG Ile His Tyr Pro Gln Leu Glu Asn Ile Ile Lys Asp Val Cys Gln Glu 315 320 325 330	2991
15	TTT GGT GTG GAA TAT AAA GTT TAT CCC ACC TTC AAA GCG GCG ATC GCC Phe Gly Val Glu Tyr Lys Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala 335 340 345	3039
	TCT AAC TAT CGC TGG CTA GAG GCC ATG GGC AAA GCA TCG TGACATTGCC Ser Asn Tyr Arg Trp Leu Glu Ala Met Gly Lys Ala Ser 350 355 360	3088
	TTGGGATTGA AGCAAAATGG CAAAATCCCT CGTAAATCTA TGATCGAAGC CTTTCTGTTG	3148
20	CCCCCGGACC AAATCCCCGA TGCTGACCAA AGGTTGATGT TGGCATTGCT CCAAACCCAC	3208
	TTTGAGGGGG TTCAATTGGCC GCAGTTTCAA GCTGACCTAG GAGGCAAAGA TTGGGTGATT	3268
	TTGCTCAAAT CCGCTGGGAT ATTGAAAGGC TTCACCACCT TTGGTTTCTA CCCTGCTCAA	3328
	TGGGAAGGAC AAACCGTCAG AATTGTTTAT TCTGGTGACA CCATCACCAG CCCATCCATG	3388
	TGGTCTAACC CAGCCCTGGC CAAGGCTTGG AÇCAAGGCCA TGCAAATTCT CCACGAGGCT	3448
25	AGGCCAGAAA AATTATATTG GCTCCTGATT TCTTCCGGCT ATCGCACCTA CCGATTTTIG	3508
	AGCATTTTTG CCAAGGAATT CTATCCCCAC TATCTCCATC CCACTCCCCC GCCTGTACAA	3568

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1 AATTTTATCC ATCAGCTAGC

3588

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Thr Ala Glu Arg Ile Lys Phe Thr Gln Lys Arg Gly Phe Arg
1 5 10 15

Arg Val Leu Asn Gln Arg Val Asp Ala Tyr Phe Ala Glu His Gly Leu
20 25 30

Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu Lys Thr Leu Ile Ile Val
35 40 45

Leu Trp Leu Phe Ser Ala Trp Ala Phe Val Leu Phe Ala Pro Val Ile
50 55 60

15 Phe Pro Val Arg Leu Leu Gly Cys Met Val Leu Ala Ile Ala Leu Ala
65 70 75 80

Ala Phe Ser Phe Asn Val Gly His Asp Ala Asn His Asn Ala Tyr Ser
85 90 95

Ser Asn Pro His Ile Asn Arg Val Leu Gly Met Thr Tyr Asp Phe Val
100 105 110

20 Gly Leu Ser Ser Phe Leu Trp Arg Tyr Arg His Asn Tyr Leu His His
115 120 125

Thr Tyr Thr Asn Ile Leu Gly His Asp Val Glu Ile His Gly Asp Gly
130 135 140

Ala Val Arg Met Ser Pro Glu Gln Glu His Val Gly Ile Tyr Arg Phe
145 150 155 160

25 Gln Gln Phe Tyr Ile Trp Gly Leu Tyr Leu Phe Ile Pro Phe Tyr Trp
165 170 175

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1 Phe Leu Tyr Asp Val Tyr Leu Val Leu Asn Lys Gly Lys Tyr His Asp
 180 185 190
 His Lys Ile Pro Pro Phe Gln Pro Leu Glu Leu Ala Ser Leu Leu Gly
 195 200 205
 5 Ile Lys Leu Leu Trp Leu Gly Tyr Val Phe Gly Leu Pro Leu Ala Leu
 210 215 220
 Gly Phe Ser Ile Pro Glu Val Leu Ile Gly Ala Ser Val Thr Tyr Met
 225 230 235 240
 Thr Tyr Gly Ile Val Val Cys Thr Ile Phe Met Leu Ala His Val Leu
 245 250 255
 10 Glu Ser Thr Glu Phe Leu Thr Pro Asp Gly Glu Ser Gly Ala Ile Asp
 260 265 270
 Asp Glu Trp Ala Ile Cys Gln Ile Arg Thr Thr Ala Asn Phe Ala Thr
 275 280 285
 Asn Asn Pro Phe Trp Asn Trp Phe Cys Gly Gly Leu Asn His Gln Val
 290 295 300
 Thr His His Leu Phe Pro Asn Ile Cys His Ile His Tyr Pro Gln Leu
 305 310 315 320
 15 Glu Asn Ile Ile Lys Asp Val Cys Gln Glu Phe Gly Val Glu Tyr Lys
 325 330 335
 Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala Ser Asn Tyr Arg Trp Leu
 340 345 350
 Glu Ala Met Gly Lys Ala Ser
 355

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1884 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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1 AGCTTCACTT CGGTTTTATA TTGTGACCAT GGTTCACAGG CATCTGCTCT AGGGAGTTTT 60
TCCGCTGCCT TTAGAGAGTA TTTTCTCCAA GTCGGCTAAC TCCCCCATTT TTAGGCAAAA 120
TCATATACAG ACTATCCCAA TATTGCCAGA GCITTGATGA CTCACTGTAG AAGGCAGACT 180
5 AAAATTCTAG CAATGGACTC CCAGTTGGAA TAAATTTTAA GTCTCCCCCG GCGCTGGAGT 240
TTTTTTGTAG TTAATGGCGG TATAATGTGA AAGTTTTTAA TCTATTTAAA TTTATAAATG 300
CTAACAGCGG AAAGAATTAA ATTTACCCAG AAACGGGGGT TTCGTCGGGT ACTAAACCAA 360
CGGGTGGATG CCTACTTTGC CGAGCATGGC CTGACCCAAA GGGATAATCC CTCCATGTAT 420
CTGAAAACCC TGATTATTGT GCTCTGGTTG TTTTCCGCTT GGGCCTTTGT GCTTTTTGCT 480
10 CCAGTTATTT TTCCGGTGCG CCTACTGGGT TGTATGGTTT TGGCGATCGC CTGGCGGGCC 540
TTTTCTTCA ATGTCGGCCA CGATGCCAAC CACAATGCCT ATTCCTCAA TCCCCACATC 600
AACCGGGTTC TGGGCATGAC CTACGATTTT GTCGGGTAT CTAGTTTTCT TTGGCGCTAT 660
CGCCACAACCT ATTTGCACCA CACCTACACC AATATCTTG GCCATGACGT GGAAATCCAT 720
GGAGATGGCG CAGTACGTAT GAGTCCTGAA CAAGAACATG TTGGTATTTA TCGTTTCCAG 780
15 CAATTTTATA TTTGGGGTTT ATATCTTTT ATTCCTTTT ATTGGTTTCT CTACGATGTC 840
TACCTAGTGC TTAATAAAGG CAAATATCAC GACCATAAAA TTCCTCCTTT CCAGCCCCTA 900
GAATTAGCTA GTTTGCTAGG GATTAAGCTA TTATGGCTCG GCTACGTTTT CGGCTTACCT 960
CTGGCTCTGG GCTTTTCCAT TCCTGAAGTA TTAATGGTG CTTGCGTAAC CTATATGACC 1020
TATGGCATCG TGGTTTGCAC CATCTTTATG CTGGCCCATG TGTTGGAATC AACTGAATTT 1080
20 CTCACCCCCG ATGGTGAATC CGGTGCCATT GATGACGAGT GGGCTATTTG CCAAATTCGT 1140
ACCACGGCCA ATTTTGCCAC CAATAATCCC TTTTGGAAC TGGTTTGTGG CGGTTTAAAT 1200
CACCAAGTTA CCCACCATCT TTTCCCAAT ATTTGTCATA TTCACTATCC CCAATTGGAA 1260
AATATTATTA AGGATGTTTG CCAAGAGTTT GGTGTGGAAT ATAAAGTTTA TCCCACCTTC 1320
AAAGCGGCGA TCGCCTCTAA CTATCGCTGG CTAGAGGCCA TGGGCAAAGC ATCGTGACAT 1380
25 TGCCTTGGGA TTGAAGCAAA ATGGCAAAAT CCCTCGTAAA TCTATGATCG AAGCCTTTCT 1440

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1 GTTGCCCGCC GACCAAATCC CCGATGCTGA CCAAAGGTTG ATGTTGGCAT TGCTCCAAAC 1500
CCACTTTGAG GGGGTTTCATT GGCCGCAGTT TCAAGCTGAC CTAGGAGGCA AAGATTGGGT 1560
GATTTTGCTC AAATCCGCTG GGATATTGAA AGGCTTCACC ACCTTTGGTT TCTACCCTGC 1620
TCAATGGGAA GGACAAACCG TCAGAATTGT TTATTCTGGT GACACCATCA CCGACCCATC 1680
5 CATGTGGTCT AAGCCAGCCC TGGCCAAGGC TTGGACCAAG GCCATGCAA TTCTCCACGA 1740
GGCTAGGCCA GAAAAATTAT ATTGGCTCCT GATTCTTCC GGCTATCGCA CCTACCGATT 1800
TTTGAGCATT TTGCCAAGG AATTCTATCC CCACTATCTC CATCCCACTC CCCC GCCTGT 1860
ACAAAATTTT ATCCATCAGC TAGC 1884

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1 WHAT IS CLAIMED:

1. An isolated nucleic acid encoding bacterial $\Delta 6$ -desaturase.

2. The nucleic acid of Claim 1 comprising the
5 nucleotides of SEQ. ID NO:3.

3. An isolated nucleic acid that codes for the amino acid sequence encoded by the nucleic acid of Claim 1.

4. The isolated nucleic acid of any one of Claims 1-3 wherein said nucleic acid is contained in a vector.

10 5. The isolated nucleic acid of Claim 4 operably linked to a promoter and/or a termination signal capable of effecting expression of the gene product of said isolated nucleic acid.

6. The isolated nucleic acid of Claim 5 wherein said
15 promoter is a $\Delta 6$ -desaturase promoter, an Anabaena carboxylase promoter, a helianthinin promoter, a glycin promoter, a napin promoter, or a helianthinin tissue-specific promoter.

7. The isolated nucleic acid of Claim 5 wherein said
20 termination signal is a Synechocystis termination signal, a nopaline synthase termination signal, or a seed termination signal.

8. The isolated nucleic acid of any one of Claims 1-7 wherein said isolated nucleic acid is contained within a transgenic organism.

25 9. The isolated nucleic acid of Claim 8 wherein said transgenic organism is a bacterium, a fungus, a plant cell or an animal.

10. A plant or progeny of said plant which has been regenerated from the transgenic plant cell of Claim 9.

30 11. The plant of Claim 10 wherein said plant is a sunflower, soybean, maize, tobacco, peanut or oil seed rape plant.

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1 12. A method of producing a plant with increased
gamma linolenic acid (GLA) content which comprises:

(a) transforming a plant cell with the isolated
nucleic acid of any one of Claims 1-7; and

5 (b) regenerating a plant with increased GLA content
from said plant cell.

13. The method of Claim 12 wherein said plant is a
sunflower, soybean, maize, tobacco, peanut or oil seed rape
plant.

10 14. A method of inducing production of gamma
linolenic acid (GLA) in an organism deficient or lacking in
GLA with comprises transforming said organism with the
isolated nucleic acid of any one of Claims 1-7.

15 15. A method of inducing production of gamma
linolenic acid (GLA) in an organism deficient or lacking in
GLA and linoleic acid (LA) which comprises transforming said
organism with an isolated nucleic acid encoding bacterial $\Delta 6$ -
desaturase and an isolated nucleic acid encoding $\Delta 12$ -
desaturase.

20 16. A method of inducing production of gamma
linolenic acid (GLA) in an organism deficient or lacking in
GLA and linoleic acid (LA) which comprises transforming said
organism with at least one expression vector comprising an
isolated nucleic acid encoding bacterial $\Delta 6$ -desaturase and an
25 isolated nucleic acid encoding $\Delta 12$ -desaturase.

17. The method of any one of Claims 15 or 16 wherein
said isolated nucleic acid encoding $\Delta 6$ -desaturase comprises
nucleotides 317 to 1507 of SEQ. ID NO:1.

30 18. A method of inducing production of
octadecatetraeonic acid in an organism deficient or lacking
in gamma linolenic acid with comprises transforming said
organism with isolated nucleic acid of any one of Claims 1-7.

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1 19. The method of Claim 18 wherein said organism is a
bacterium, a fungus, a plant or an animal.

 20. A method of use of the isolated nucleic acid of
any one of Claims 1-7 to produce a plant with improved
5 chilling resistance which comprises:

 a) transforming a plant cell with the isolated
nucleic acid of any one of Claims 1-7; and

 b) regenerating said plant with improved chilling
resistance from said transformed plant cell.
10 21. The method of Claim 20 wherein said plant is a
sunflower, soybean, maize, tobacco, peanut or oil seed rape
plant.

 22. Isolated bacterial $\Delta 6$ -desaturase.

 23. The isolated bacterial $\Delta 6$ -desaturase of Claim 22
15 which has an amino acid sequence of SEQ ID NO:2.

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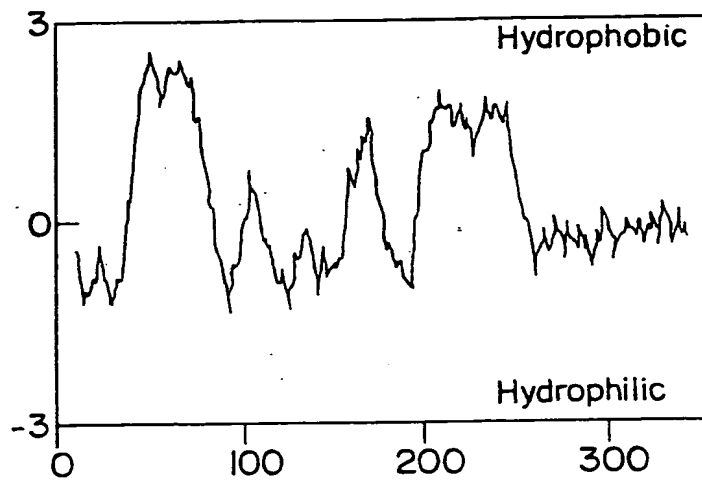


FIG. 1A

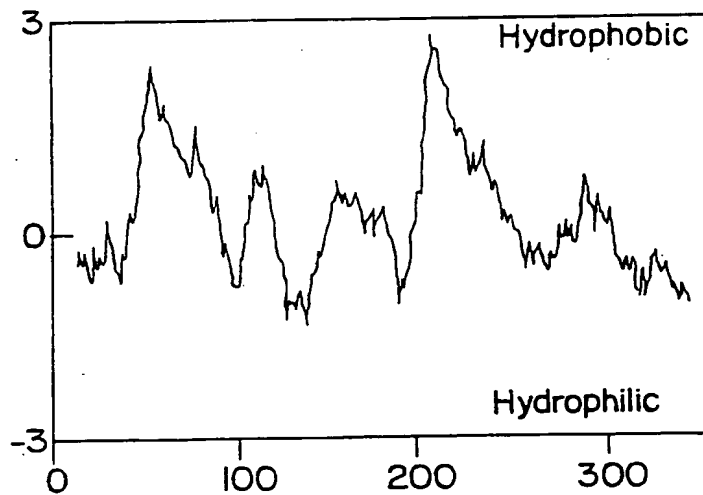


FIG. 1B

FIG. 2A

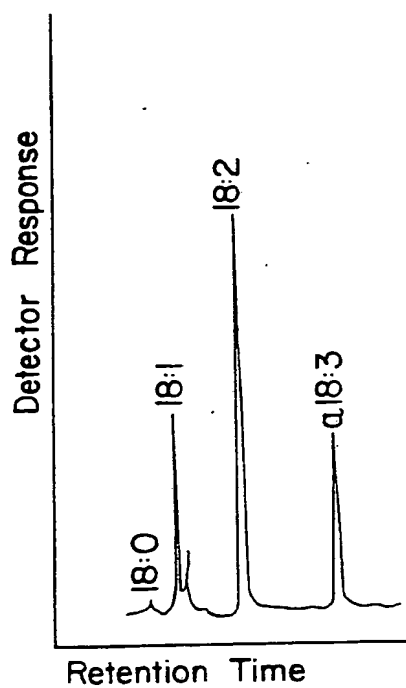


FIG. 2B

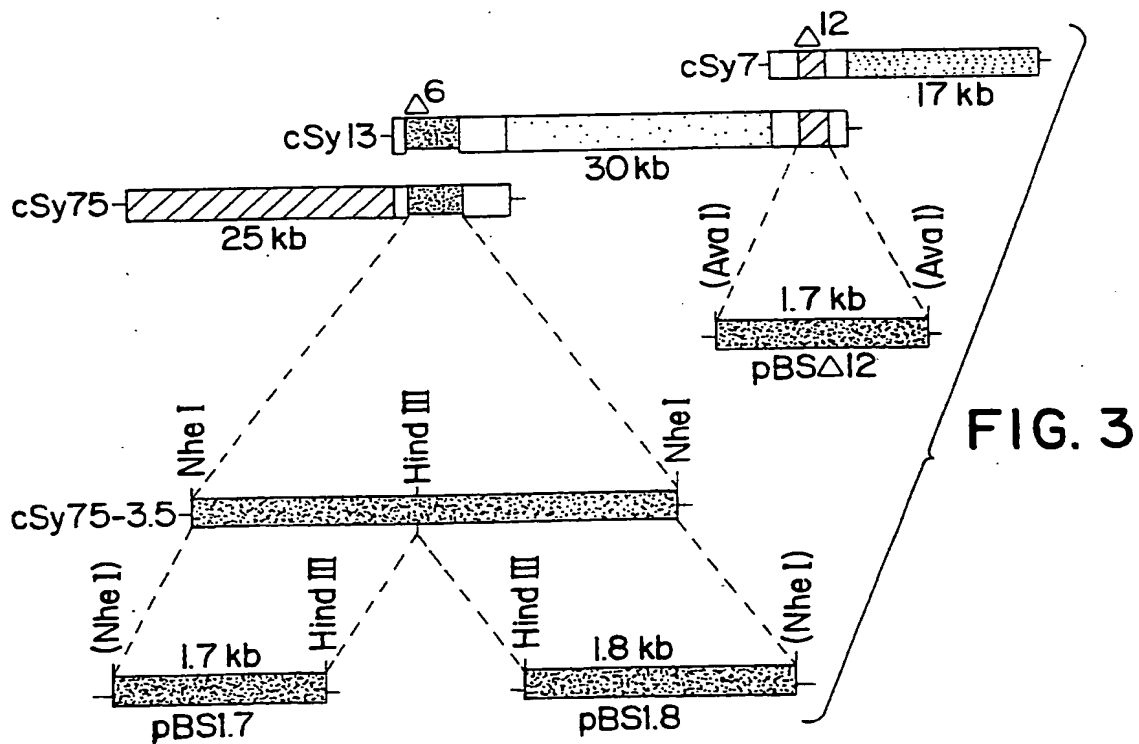
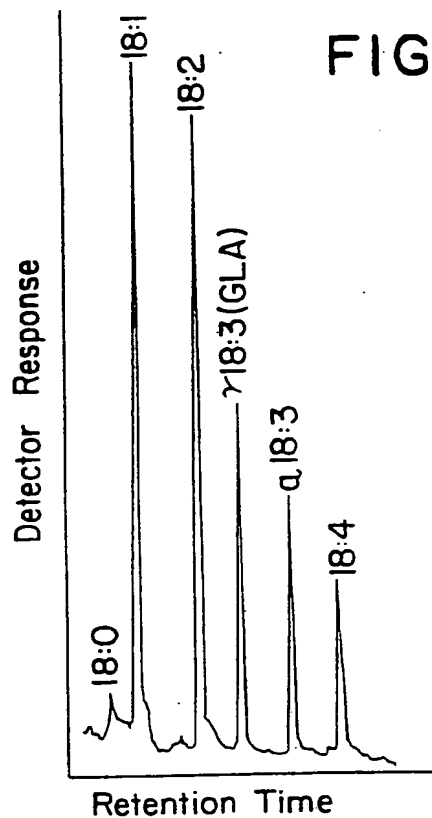


FIG. 3

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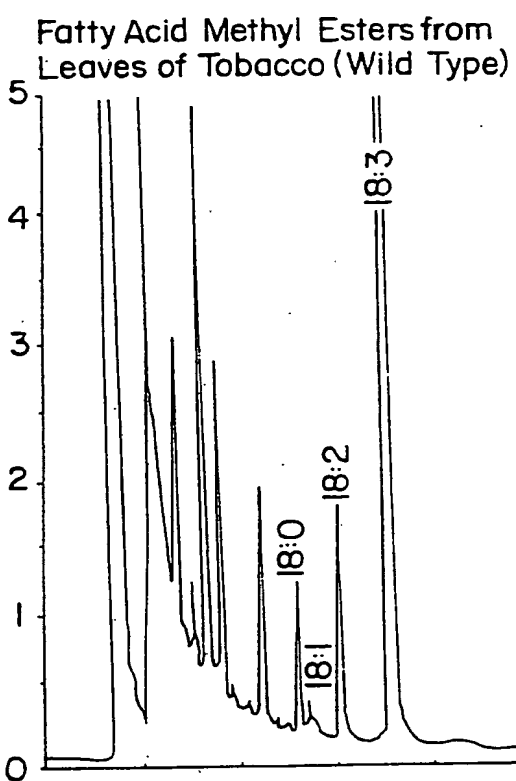


FIG. 4A

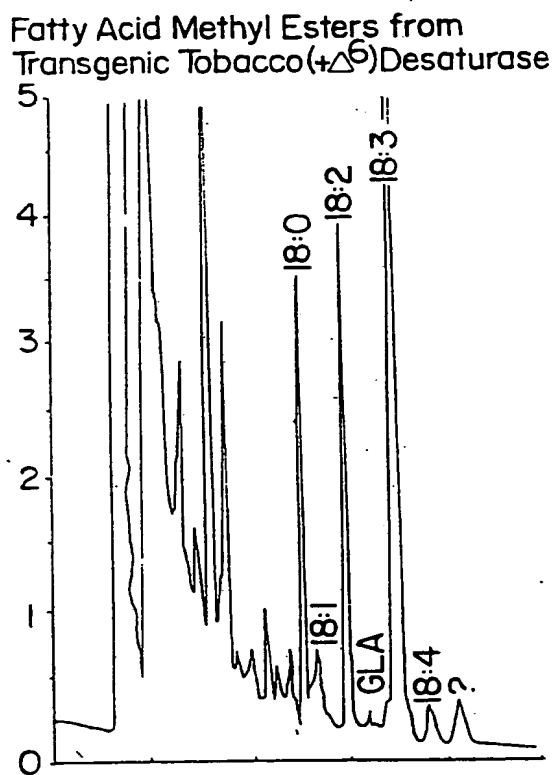


FIG. 4B

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/US92/08746

A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) : Please See Extra Sheet.

US CL : 800/205; 435/172.3, 189, 69.1, 320.1, 134, 170, 171; 536/27

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 800/205; 435/172.3, 189, 69.1, 320.1, 134, 170, 171; 536/27;
935/9, 30, 6, 24, 29, 38

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN/BIOSIS, CA; APS

search terms: linolenic, desaturase, delta-6, gene, DNA, cDNA,
purif?, cyanobacteri?,**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Nature, Volume 347, issued 13 September 1990, H. Wada et al., "Enhancement of Chilling Tolerance of a Cyanobacterium by Genetic Manipulation of Fatty Acid Desaturation", pages 200-203, especially pages 201-203.	1-23
Y	Biochemical Journal, Volume 240, issued 1986, S. Stymne et al., "Biosynthesis of γ -Linolenic Acid in Cotyledons and Microsomal Preparations of the Developing Seeds of Common Borage (<i>Borago officinalis</i>)", pages 385-392, especially pages 385 and 392.	1-23
Y	EP, A, 0,255, 378 (Kridl et al.) 3 February 1988, see entire document, especially columns 3-5 and 7-11.	1-23

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

•	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"G"	document member of the same patent family

Date of the actual completion of the international search

03 DECEMBER 1992

Date of mailing of the international search report

13 JAN 1993

Name and mailing address of the ISA/
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. NOT APPLICABLE

Authorized officer

CHARLES C. P. RORIES, PH.D.

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US92/08746

A. CLASSIFICATION OF SUBJECT MATTER: IPC (5):

A01H 1/00, 5/00; C12N 15/00, 9/02; C12P 7/64, 1/02, 1/04, 21/06; C07H 15/12, 17/00

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